

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Roger  
Au-Young, Janice  
Bandman, Olga  
Seilhammer, Jeffrey
- (ii) TITLE OF INVENTION: THROMBIN RECEPTOR HOMOLOG
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: INCYTE GENOMICS, INC.  
(B) STREET: 3160 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: FastSeq for Windows Version 2.0
- (vi) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/217,101  
(B) FILING DATE: 21-DEC-1998
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/911,320  
(B) FILING DATE: August 14, 1997
- (viii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/467,125  
(B) FILING DATE: 6-JUN-1995
- (ix) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Billings, Lucy J.  
(B) REGISTRATION NUMBER: 36,749  
(C) REFERENCE/DOCKET NUMBER: PF-0041-3 DIV
- (x) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-845-4170  
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1143 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: Liver  
(B) CLONE: 86700

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGAAGTC	ATACCATAAC	AATGACGACA	ACTTCAGTCA	GCAGCTGGCC	TTACTCCTCC	60
CACAGAATGC	GCTTTATAAC	CAATCATAGC	GACCAACCGC	CACAAAACCT	CTCAGCAACA	120
CCAAATGTTA	CTACCTGTCC	CATGGATGAA	AAATTGCTAT	CTACTGTGTT	AACCACATCC	180
TACTCTGTTA	TTTTCATCGT	GGGACTGGTT	GGGAACATAA	TCGCCCCCTA	TGTATTTCTG	240
GGTATTCACC	GTAAGAAGAA	TTCCATTCAA	ATTTATCTAC	TTAACGTAGC	CATTGCAGAC	300
CTCCTACTCA	TCTTCTGCCT	CCCTTTCCGA	ATAATGTATC	ATATTAACCA	AAACAAGTGG	360
ACACTAGGTG	TGATTCTGTT	CAAGGTTGTG	GGAACACTGC	TTTATATGAA	CATGTACATT	420
AGCATTATTT	TGCTTGGATT	CATCAGTTTG	GATCGCTATA	TAAAAATTAA	TCGGTCTATA	480
CAGCAACGGA	AGGCAATAAC	AACCAACAA	AGTATTTATG	TCTGTTGTAT	AGTATGGATG	540
CTTGCTCTTG	GTGGATTCCCT	AACATATGAT	ATTTTAACAC	TTAAGAAAGG	AGGGCATAAT	600
TCCACAATGT	GTTTCCATTA	CAGAGATAAG	CATAACGCAA	AAGGAGAAGC	CATTTTAAAC	660
TTTATCTCTG	TGGTAAGTGT	CTGGCTAATT	TTCTTACTAA	TAATCCTTTC	ATATATTAAG	720
ATTGGGAAGA	ATCTATTGAG	GATTTTCTAAA	AGGAGGTCAA	AAATTTCTAA	TTCTGGTAAA	780
TATGCCACATA	CAGCTCGTAA	CTCCTTTTAT	GTACTTATCA	TTTTTACTAT	ATGTGTGGGT	840
CCCTATCATG	CGTTTTCGATT	CATCTACATT	TCTTCACAGC	TAAATGTATC	ATCTGTCTAC	900
TGGAAAGAAA	TTGTTTCACAA	AACCAATGAG	ATCATGCTGG	TTCTCTCATC	TTTCAATAGT	960
TGGTTAGATC	CAGTCATGTA	TTTCTGTATG	TCCAGTAACA	TTGCGAAAAA	AATGTGCGAA	1020
CTTCTTTTAA	GACGATTTCA	AGGTGAACCA	AGTAGGAGTG	AAAGCACTTC	AGAATTTAAA	1080
CCAGGATACT	CCCTGCATGA	TACATCTGTG	GCAGGAAAAA	TACAGTCTAG	TTCTGAAAGT	1140
ACT						1143

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 381 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Ser	His	Thr	Ile	Thr	Met	Thr	Thr	Ser	Val	Ser	Ser	Trp
1				5					10				15	
Pro	Tyr	Ser	Ser	His	Arg	Met	Arg	Phe	Ile	Thr	Asn	His	Ser	Asp
				20				25					30	Gln
Pro	Pro	Gln	Asn	Phe	Ser	Ala	Thr	Pro	Asn	Val	Thr	Thr	Cys	Pro
				35			40					45		Met
Asp	Glu	Lys	Leu	Leu	Ser	Thr	Val	Leu	Thr	Thr	Ser	Tyr	Ser	Val
				50			55				60			Ile
Phe	Ile	Val	Gly	Leu	Val	Gly	Asn	Ile	Ile	Ala	Pro	Tyr	Val	Phe
														Leu

65		70		75		80
Gly	Ile	His	Arg	Lys	Arg	Asn
		85		90		95
Ala	Ile	Ala	Asp	Leu	Leu	Leu
		100		105		110
Tyr	His	Ile	Asn	Gln	Asn	Lys
		115		120		125
Val	Val	Gly	Thr	Leu	Leu	Tyr
		130		135		140
Leu	Gly	Phe	Ile	Ser	Leu	Asp
		145		150		155
Gln	Gln	Arg	Lys	Ala	Ile	Thr
		165		170		175
Ile	Val	Trp	Met	Leu	Ala	Leu
		180		185		190
Thr	Leu	Lys	Lys	Gly	Gly	His
		195		200		205
Asp	Lys	His	Asn	Ala	Lys	Gly
		210		215		220
Val	Met	Phe	Trp	Leu	Ile	Phe
		225		230		235
Ile	Gly	Lys	Asn	Leu	Leu	Arg
		245		250		255
Asn	Ser	Gly	Lys	Tyr	Ala	Thr
		260		265		270
Ile	Ile	Phe	Thr	Ile	Cys	Val
		275		280		285
Tyr	Ile	Ser	Ser	Gln	Leu	Asn
		290		295		300
Val	His	Lys	Thr	Asn	Glu	Ile
		305		310		315
Trp	Leu	Asp	Pro	Val	Met	Tyr
		325		330		335
Ile	Met	Cys	Gln	Leu	Leu	Phe
		340		345		350
Ser	Glu	Ser	Thr	Ser	Glu	Phe
		355		360		365
Ser	Val	Ala	Gly	Lys	Ile	Gln
		370		375		380

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys

1	5	10	15
Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys			
20	25	30	
Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro			
35	40	45	
Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser			
50	55	60	
Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu			
65	70	75	80
Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu			
85	90	95	
Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val			
100	105	110	
Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile			
115	120	125	
Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu			
130	135	140	
Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser			
145	150	155	160
Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg			
165	170	175	
Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu Leu			
180	185	190	
Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met			
195	200	205	
Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu			
210	215	220	
Ala Ile Trp Ala Leu Ala Ile Ala Gly Val Val Pro Leu Val Leu Lys			
225	230	235	240
Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr Cys His Asp			
245	250	255	
Val Leu Asn Glu Thr Leu Leu Glu Gly Tyr Tyr Ala Tyr Tyr Phe Ser			
260	265	270	
Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu Ile Ile Ser Thr Val			
275	280	285	
Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ser Ala Val Ala Asn			
290	295	300	
Arg Ser Lys Lys Ser Arg Ala Leu Phe Leu Ser Ala Ala Val Phe Cys			
305	310	315	320
Ile Phe Ile Ile Cys Phe Gly Pro Thr Asn Val Leu Leu Ile Ala His			
325	330	335	
Tyr Ser Phe Leu Ser His Thr Ser Thr Thr Glu Ala Ala Tyr Phe Ala			
340	345	350	
Tyr Leu Leu Cys Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro			
355	360	365	
Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser			
370	375	380	
Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser			
385	390	395	400
Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn			
405	410	415	
Asn Ser Ile Tyr Lys Lys Leu Leu Thr			
420	425		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

AAGGAGGGCATAATTCACAATGTG

(25)

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

AAGGAGGGCATAATTCACAATGTG

(25)